



Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
Applicant(s): Robert G. Korneluk et al.
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HUMAN xiap

BEST AVAILABLE COPY

HUMAN xiap

361 atccagaatggtcagtaaaaaactatctggaaaggcagatcattttgcctta 420
a I Q N G Q Y K V E N Y L G S R D H F A L -
421 gacaggccatctgagacacatgcagactatctttgagaactggcaggttgttagatata 480
a D R P S E T H A D Y L L R T G Q V V D I -
481 tcagacaccatatacccgaggaaccctgcccattgttgaagaaggcttagattaaaggcc 540
a S D T I Y P R N P A M Y C E E A R L K S -
541 ttccagaactggccagactatgctcacctaaccccaaggagaggtttagcaaggctggactc 600
a F Q N W P D Y A H L T P R E L A S A G L -
601 tactacacaggattggtgcaccaaggcagttgcaggctttgtgtggaaaactgaaaaat 660
a Y Y T G I G D Q V Q C F C C G G K L K N -
661 tgggaaccttgtgatcggtgcctgttcagaacacaggcgcacactttcctaattgcttt 720
a W E P C D R A W S E H R R H F P N C F F -

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HUMAN xiap

Fig. 1 (page 3 of 7)

HUMAN xiap

1081	a	gagggtctggtaagaaactactgagaaaacaccatcactaaactagaagaattgtatgatacc	1140
1141	a	atcttccaaaatccatatggtacaagaagctatacgaatggggttcagttcaaggacatt	1200
1201	a	I F Q N P M V Q E A I R M G F S F K D I - aagaaaataatggagggaaaaattcagatattctggggaggcaactataaattcacttggaggtt	1260
1261	a	K K I M E E K I Q I S G S N Y K S L E V - ctgggtgcagatcttagtgaatgtcagaaaggacagtcagttcaaggatgaggtaaggtcagact	1320
1321	a	L V A D L V N A Q K D S M Q D E S S Q T - tcattacagaaaggattagtactgaaaggcagctaaaggcgccctgcaaggaggaaaggctt	1380
1381	a	S L Q K E I S T E E Q L R R L Q E E K L - tgccaaaatctgtatggatagaaataattgctatacgttttgtggacatcttagtc	1440

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HUMAN xiap

1801 attcatgtataactgatttaaattctaaggtaaagtgttaatcatctggatttttat - + 1860
a
1861 tctttcagataggcttaacaaatggagcttctgttatataatgtggagatttaggtta - + 1920
a
1921 atctccccaaatcacataatttgttttgtgaaaaaggaaataaaattgttccatgctggtg - + 1980
a
1981 gaaagatagagatgttttagaggttgggttgtgttttaggattctgtccattttct - + 2040
a
2041 tgtaaagnataaacacgnaacntgtcgaaatataatgtaaagtgttgcatttttg - + 2100
a
2101 aaagcgtatttaatgatagaataactatcgaggccaaacatgtactgacatggaaaggatgtca - + 2160
a

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HUMAN xiap

2161 - nagatatgttaagtgtaaaatgcaaggtaggcnnnacactatgtatagtcgtagccagatca 2220
a -
2221 - aagtatgttatgttttaatatgcatagaacnananagatttggaaagatacacccaaactg 2280
a -
2281 - ttaaatgtgggtttcttcggggggggattggggggcccaaggagggtttta 2340
a -
2341 - naggggccctttcacttttcaactttttcatttttttttttttataaagtat 2400
a -
2401 - gtnaccnnaagggtttatggnaactaaacatcagtaaccctaaaccccggtgactatcc 2460
a -
2461 - gtnctttcccttagggaggctgtntttcccaaccctttccctgtgaaccaaatgc 2520
a -
2521 - ctgagtgtggggcactttn 2540
a -

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HUMAN hiap-1

SEQ ID NO: 5	1	TCCTTGAGATGTTAGGATTCAGTATAGGATCTCCATGTTGGAACTCTAAATGCATAGA	60
		C	
	61	AATGGAAATAATGGAATTTCATTGGCTTTCAGCCTAGTATAAAACTGATAAAA	120
		C	
	121	GCAAAGGCCATGCCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTCTTCCCCATTG	180
		C	
	181	ATTTCATTATGAAACATAGTAGAAAACAGCATATTCTTATCAAATTGATGAAAAGGCCA	240
		SEQ ID NO: 6	
		C	
	241	ACACGTTTGAACCTGAAATAACGACTTGTCAATGTGAACCTGAAATGTCTACGTATTCCA	300
		C	
	301	T F E I K Y D L S C E I Y R M S T Y S T - CTTTCTGCTGGGGTCCCTGTCAGAAAGGAGTCTTGCTCGTGGTTCTATTACA	360
		C	

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HUMAN hiap-1

361	CTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGGCCTGATGGATAACTGGAAAA	420
C	G V N D K V C F C C G L M L D N W K R -	
	GAGGAGACAGTCCTACTGAAAAGCATAAAAGTTGTATCCTAGCTGCAGATTGTTCAAGA	
421		480
C	G D S P T E K H K L Y P S C R F V Q S -	
	GTCTAAATTCCGTTAACAACTTGAAGCTAACCTCTCAGCC"ACTTTCTTCTTCAGTAA	
481		540
C	L N S V N N L E A T S Q P T F P S S V T -	
	CACATTCCACACACTCATTACTTCCGGTACAGAAAACAGTGGATATTCCGGCTCTT	
541		600
C	H S T H S L L P G T E N S G Y F R G S Y -	
	ATTCAAACCTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTCCTG	
601		660
C	S N S P S N P V N S R A N Q E F S A L M -	
	TGAGAAGTTCCCTACCCCTGTCCCAATGAAATACGAAAATGCCAGATTACTTACTTCAAGA	
661		720
C	R S S Y P C P M N N E N A R L L T F Q T -	

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HUMAN hiap-1

C	721	CATGGCCATTGACTTTCTGTCGCCAACAGATCTGGCACGAGCAGGCTTTACTACATAG	780
C	781	W P L T F L S P T D L A R A G F Y Y I G -	
C	841	GACCTGGAGACAGAGTGGCTTGCTTGCCTGTGGTGGAAATTGAGCAATTGGAAACCGA	840
C	901	P G D R V A C F A C G G K L S N W E P K -	
C	961	AGGATAATTGCTATGTCAGAACACCTGAGACATTTCCTCAAATGCCATTATAGAAAATC	900
C	1021	D N A M S E H L R H F P K C P F I E N Q -	
C		AGCTTCAAGACACACTTCAAGATAACACAGTTCTAATCTGAGCATGCAGACACATGCAGCCCC	960
C		L Q D T S R Y T V S N L S M Q T H A A R -	
C		GCTTTAAACATTCTTTAACACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCCTTGCAA	1020
C		F K T F F N W P S S V L V N P E Q L A S -	
C		GTGGGGTTTATTATGTGGTAACAGTGTATGTCAAATGCTTTGCTGTGATGGTG	1080
C		A G F Y Y V G N S D D V K C C D G G -	

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HUMAN hiap-1

1081	CACTCAGGGTGGGAATCTGGAGATGATCCATGGGTCAACATGCCAAGTGGTTCCAA	1140
c	L R C W E S G D D P W V Q H A K W F P R -	
1141	GGTGTGAGTACTTGATAAGAATTAAAGGACAGGGAGTTCATCCCGTCAAGTTCAAGGCCAGTT	1200
c	C E Y L I R I K G Q E F I R Q V Q A S Y -	
1201	ACCCCTCATCTACTTGAAACAGCTGCTATCCACATCAGACAGGCCAGGAGATGAAATGCAG	1260
c	P H L L E Q L L S T S D S P G D E N A E -	
1261	AGTCATCAATTATCCATTGGAACCTGGAGAAGACCCATTCAAAGATGCAATCATGATGAA	1320
c	S S I I H L E P G E D H S E D A I M M N -	
1321	ATACTCCCTGATTAAATGCTGCCGTGGAAATGGCTTTAGTAGAAGGCCCTGGTAAACAGA	1380
c	T P V I N A A V E M G F S R S L V K Q T -	
1381	CAGTCAGAGAAAATCCTAGCAACCTGGAGAGAAATTAGACTAGTCATGATCTTGTGT	1440
c	V Q R K I L A T G E N Y R L V N D L V L -	

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HUMAN hiap-1

1801	ATGTTTCAAGATCTTACCAAGTGGAAAGAACAAATTGGGGAGACTACCAAGAAGAACATGTA	1860
C	V S D L P V E E Q L R R I P E E R T C K -	
1861	AAGTGTGTATGGACAAAGAACATAGTGTCCATAGTGTATTCTGGTCATCTAGTAGTAT	1920
C	V C M D K E V S I V F I P C G H L V V C -	
1921	GCAGGATTGTGCTCCCTTTAGAAAGTGTCCATTGAGGTACAATCAAGGGTA	1980
C	K D C A P S L R K C P I C R S T I K G T -	
1981	CAGTCGTACATTTCTTCATGAGAACCAAAACATCGTCTAAACTTGAATTAAAT	2040
C	V R T F L S *	-
2041	TTATTAATGTATTATAACTTTAACCTTATCCTAATTGGTTCCCTAAATTTTATT	2100
C	-	
2101	TATTACAACTCAAAACATTGTTTGTGTAACATATTATATGTATCTAAACCATA	2160
C	-	

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HUMAN hiap-1

2521	CAGTGTCCATTACATCGAAGGTGTGCATATATGTTGAATCACATTAGGGACATGGTGT	-	2580
2581	TTTTATAAGAATTCTGTGAGXAAAAATTAAATAAGCAACCXAAATTACTCTTAAAAAA	-	2640
2641	AAAAAAAAAAACTCGAGGGCCCCGTACCAAT	-	2676

Fig. 2 (page 8 of 8)

HUMAN hiap-2

SEQ ID NO: 7 1 TTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTTCTAAGTAGGTATCTTGG
a -
61 TAATTCAGAGAGATACTCATCCTACCTGAATAAACTGAGATAAAATCCAGTAAAGAAAG
a -
121 TGTAGTAAATTCTACATAAGAGTCTATCATTGATTCTTGTGGAAATCTTAGTT
a -
181 CATGTGAAGAAATTTCATGTGAATGTTTAGCTATCAAACAGTACTGTCACCTACTCATG
a -
241 CACAAAAGACTGCCAAAGACTTTCCCAAGGTCCCTCGTATCAAACATTAGAGTATA
a M -
301 ATGGAAGATAGCACGATCTTGTCAAGATTGGACAAACAGCAACAAACAAAAATGAAGTAT
a M E D S T I L S D W T N S N K Q K M K Y -

SEQ ID NO: 8 a H K T A S Q R L F P G P S Y Q N I K S I -
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HUMAN hiap-2

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HUMAN hiap-2

		ATTCTAGGAGTTGAAGGACATCTTCA	TGAGGACTAACCCCTACAGTTATGCAATG		
721	a	N S R A V E D I S S S R T N P Y S Y A M -			780
		AGTACTGAAGAACCCAGATTTCTTACCATATGGCCATTAACTTTGTCACCA			
781	a	S T E E A R F L T Y H M W P L T F L S P -			840
		TCAGAATTGGCAAGAGCTGGTTTATTATAGGACCTGGAGATAGGGTAGGCCCTGCTT			
841	a	S E L A R A G F Y Y I G P G D R V A C F -			900
		GCCTGTGGTGGAAAGCTCAGTAACGGAAACCAAAGGATGATGCTATGTCAGAACCCGG			
901	a	A C G G K L S N W E P K D D A M S E H R -			960
		AGGCATTTCACCAACTGTCCATTGGAAAATTCTCTAGAAACTCTGAGGTTAGCAT			
961	a	R H F P N C P F L E N S L E T L R F S I -			1020
		TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTTACTGCCATCT			
1021	a	S N L S M Q T H A A R M R T F M Y W P S -			1080

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HUMAN hiap-2

2161 ATCTAAAGTAAAGGAAATTATGAGTTTCAATTAGTAACATTCAATGTTCTAGTCTGC 2220
a
2221 TTTGGTACTAATAATCTTGTTCCTGAAAAGATGGTATCATATTAACTTAACTCTGT 2280
a
2281 TATTACAAGGAAAGATTATGTTGGTGAACCTATTAGTATGTATGGTACCTAACGGG 2340
a
2341 AGTAGCCGTCXCTGCTTGTATGCCATCATTTCAAGGAGTTACTGGATTGGTTTCAG 2400
a
2401 AAAGCTTGAAXACTAAATTATAGTGTAGAAAAGAACCTGGAAACTCTGGAGTT 2460
a
2461 CATCAGACTTATGGTGCCGAATTGCTTTGGTGCCTTCACTTGTGTTAAATAAGGA 2520
a
2521 TTTTTCTCTTATTCTCCCTAGTTGTGAGAAACATCTCAATAAGTGCCTTAAAGG 2580
a

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MOUSE xiap

SEQ ID NO:9 1 GACACTCTGCTGGGGGGGGGGGGGGGGGGACCTCCGGAAACCGGTCGCC 60
a
-
a
61 GCGGCCTTAGGACTGGAGTGCTTGGCGCGAAAAGGGGACAAGTCCTATTCCA 120
a
-
a
121 GAGAAGATGACTTTAACAGTTGAAGGAACTAGAACCTTGTACTTGGAGACCAAT 180
a
-
a
181 AAGGATGAAATTGAGAAGAGTTAATAGATTAAAAACATTGCTAACTTCCCAAAGT 240
a
K D E E F V E E F N R L K T F A N F P S -
a
241 AGTAGTCCTGTTTCAGCATCAACATTGGCGGAGCTGGTTTATACCGGTGAAGGA 300
a
-
a
301 GACACCGTGGCAATGTTCAAGTTGTCATGGGGCAATAGATAGATGGGAGACTCA 360
a
D T V Q C F S C H A A I D R W Q Y G D S -

Fig. 4 (page 1 of 6)

MOUSE xiap

361	GCTGTTGGAAGACACAGGAGAATATCCCCAAATTCCAGATTATCAATGGTTTTATT	420
a	A V G R H R R I S P N C R F I N G F Y F -	
421	GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA	480
a	E N G A A Q S T N P G I Q N G Q Y K S E -	
481	AACTGTGTGGAAATAGAAATCCTTTGCCCCCTGACAGGCCACCTGAGACTCATGCTGAT	540
a	N C V G N R N P F A P D R P P E T H A D -	
541	TATCTCTTGAGAACTGGACAGGTGTAGATATTTCAGACACCATATAACCCGAGGAACCC	600
a	Y L L R T G Q V V D I S D T I Y P R N P -	
601	GCCATGTGTAGTGAAGAACCCAGATTGAAGTCATTTCAGAACTGGCTCAT	660
a	A M C S E E A R L K S F Q N W P D Y A H -	
661	TTAACCCCCAGAGAGTTAGTGTAGCTAGTGGCTCTACTACACAGGGGCTGATGGATCAAGTG	720
a	L T P R E L A S A G L Y Y T G A D D Q V -	

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MOUSE xiap

	CAATGCTTTTGTGGGGAAACTGAAAATTGGGAACCCCTGTGATCGTGCCTGGTCA	780
a	Q C F C C G G K L K N W E P C D R A W S -	721
	GAACACAGGAGACACTTCCCAATTGGCTTTGGTTGGCCGGAACGTTAATGTTCGA	840
a	E H R R H F P N C F F V L G R N V N V R -	781
	AGTGAATCTGGTGTGAGTTCTGATAAGGAATTCCAAATTCAACAAACTCTCCAAGAAAT	900
a	S E S G V S S D R N F P N S T N S P R N -	841
	CCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTGGAACATGGATATACTCAGTT	960
a	P A M A E Y E A R I V T F G T W I Y S V -	901
	AACAAGGAGCAGCTTGCAAGAGCTGGATTATGCTTTAGGTGAAGGGATAAAGTGAAG	1020
a	N K E Q L A R A G F Y A L G E G D K V K -	961
	TGCTTCCACTGTGGAGGGGGCTCACGGATGGAAAGCCAAGTGAAGACCCCTGGGACCAAG	1080
a	C F H C G G G L T D W K P S E D P W D Q -	1021

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MOUSE xiap

1081	CATGGCTAAGTGCTACCCAGGGTGC	AAATAACCTTATGGATGAGAAGGGCAAGAAATATA	1140
a	H A K C Y P G C K Y L L D E K G Q E Y I	-	
1141	AATAATATTCA	TTAACCCATCCACTTGAGGAATCTTGGGAAGAACTGCTGAAAAAACA	1200
a	N N I H L T H P L E E S L G R T A E K T	-	
	CCACCGCTAACTAA	AAATGGATGATAACCCTTCAGAACCTTATGGTGCAGAGGCT	
1201	P P L T K K I D D T I F Q N P M V Q E A	-	1260
a	ATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAATCCAAACA	-	1320
1261	I R M G F S F K D L K T M E E K I Q T	-	
a	TCCGGAGCAGCTATCACTTGAGGTCCCTGATTGAGATCTTGTGAGTCAGAAA		
1321	1380		
a	S G S S Y L S L E V L I A D L V S A Q K	-	
1381	GATAATACGGAGGATGAGTCAA	ACTTCATTGCAGAAAGACATTAGTACTGAAGAG	1440
a	D N T E D E S S Q T S L Q K D I S T E E	-	

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MOUSE xiap

1441	a	CAGCTAAGGGCCTACAAGAGGAGCTTCCAAAATCTGTATGGATAGAAATAATTGCT	1500
		Q L R R L Q E E K L S K I C M D R N I A -	
		ATCGTTTCTTGCACATCTGGCCCACTTGTAAACAGTGTGCAGAAGGCAGTTGAC	1560
1501	a	I V F F P C G H L A T C K Q C A E A V D -	
		AAATGTCCCCATGTGCTAACCGGTCAATTACGTTCAACCAAAAATTTTATGCTTAGTGG	1620
1561	a	K C P M C Y T V I T F N Q K I F M S * -	
		GGCACACATGTTATGTTCTTGCTCTAATTGAATGTGTAATGGGAGGAACTTAAAG	1680
1621	a	-	
		TAATCCTGCATTGCATTCCATTAGCATCCTGCTGTTCCAATGGAGACCAATGCTAAC	1740
1681	a	-	
		AGCACTGTTCCGGTCTAAACATCAATTCTGATCTGGATCTTGCAGTTATCAGCTGTATCATT	1800
1741	a	-	

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MOUSE Xiap

1801	TAGCCAGTGTTTACTCGATTGAAACCTTAGACAGAGCATTATAGCTTTCACAT	-	1860
a		-	
1861	GTATATTGGTAGTACACTGACTTGTATTCTATATGTAAGTGAATTCACTGCATGTT	-	1920
a		-	
1921	TCATGCCTTTGCATAAGCTAACAAATGGAGTGTTCGTATAAGCATGGAGATGTGATG	-	1980
a		-	
1981	GAATCTGCCCAATGACTTTAACCTGGCTTATTGTAACACCGGAAAGAACTGCCAACGCTG	-	2040
a		-	
2041	CTGGGAGATAAAAGATTGTTTAGATGCTCACTTCTGTGTTAGGATTCTGCCATTAA	-	2100
a		-	

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M-hiap-1

SEQ ID NO: 39	GAATTCCGGAGACCTACACCCCCGGAGATCAGAGGTCAATTGCTGGCGTTCAAGAGCCTAG		
1	- - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	60	
61	GAAGTGGGCTGGGTATCAGGCCCTAGCAGTAAACCGACAGAAGCCATGGCACAAAACATAC	- - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	120
121	ATCCCCAGAGAAAGACTTGTCCCTTCCCTGTICATCTCACCATGAAACATGGTTCAA	- - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	180
	SEQ ID NO: 40	M N M V Q -	
181	GACAGGCCCTTTCTAGCCAAGCTGATGAAGAGTGCCTGACACCCCTTGAGTTGAAGTATGAC	+ - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	240
241	TTTCCCTGTGAGCTGTACCGATTGCCACGTATTCAAGCTTTCCAGGGAGTTCTGTGT	+ - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	300
301	TCAGAAAGGAGTCTGGCTCGTGGCTTACTACACTGGCCAATGACAAGGTCAG	+ - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	360
361	TGCTTCTGGCTGTGGCTGATGCTAGACAACACTGGAAACACAAGGGACAGTCCCATGGAGAAG	+ - - - + - - - + - - - + - - - + - - - + - - - + - - - + - - - + -	420
	C F C C G L M L D N W K Q G D S P M E K -		

Fig. 5 (page 1 of 6)

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M-hiap-1

421	CACAGAAAGTTGTACCCCCAGCTGGCAACTTGTACAGACTTGTGAATCCAGCCAAACAGTCTG	480
	H R K L Y P S C N F V Q T L N P A N S L -	
481	GAAGCTAGTCCTCGGCCCTTCTCTCTCACGGCGATGAGCACCATGCCCTTGAGCTT	540
	E A S P R P S L P S T A M S T M P L S F -	
541	GCAAGTTCTGAGAAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCTCAGACCC	600
	A S S E N T G Y F S G S Y S S F P S D P -	
601	GTTGAACCTCCGAGCAAATCAAAGATTGTCCTGCTTGTGAGCACAAAGTCCCTACCAACTTTGCA	660
	V N F R A N Q D C P A L S T S P Y H F A -	
661	ATGAAACACAGAGAAAGGCCAGATTACTCACCTATGAAACATGCCATTGTCTTCTGTCA	720
	M N T E K A R L L T Y E T W P L S F L S -	
721	CCAGCAAAGCTGGCCAAAGCAGGGCTCTACTACATAGGACCTGGAGATAGAGTGGCCTGCG	780
	P A K L A K A G F Y Y I G P G D R V A C -	

Fig. 5 (page 2 of 6)

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M-hiap-1

781	T T G C G T G C G A T G G G A A C T G A G C C A A C T G G G A A C G T A A G G A T G A T G C T A T G T C A G A G C A C	840
	F A C D G K L S N W E R K D D A M S E H -	
	C A G A G G C A T T C C C C A G G T G T C C G T C T C T A I L K G A C T T G G G T C A G T C T G C T G A G A T A C	
841	Q R H F P S C P F L K D L G Q S A S R Y -	900
	A C T G T C T C T A A C C T G A G C A T G C A G A C A C A C G C A G C C C G T A T T A G A A C A C T T C T C T A A C T G G	
901	T V S N L S M Q T H A A R I R T F S N W -	960
	C C T T C T A G T G C A C T A G T T C A T T C C A G G A A C T T G C A A G T G C G G C T T T A T T A C A G G A	
961	P S S A L V H S Q E L A S A G F Y Y T G -	1020
	C A C A G T G A T G T C A A G T G T T T A T G C T G A T G G T G G G C T G A G G T G C T G G G A A T C T G G A	
1021	H S D V K C L C C D G G L R C W E S G -	1080
	G A T G A C C C C T G G G T G G A A C A T G C C A A G T G T T C C A A G G T G T G A G T C A T T G C T C A G A A T C	
1081	D D P W V E H A K W F P R C E Y L L R I -	1140
	A A A G G C C A A G A A T T T G T C A G G C C A A G T T C A A G G C T G G C T A T C C T C A T C T G A G G C G C T A	
1141	K G Q E F V S Q V Q A G Y P H L L E Q L -	1200

Fig. 5 (page 3 of 6)

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M-hiap-1

1201	TTATCTACGTCAAGACTCCCCAGAAGATGAGAATGCGAGACGGACAAATCGTGCATTGGC	1260
L S T S D S P E D E N A D A A I V H F G -		
1261	CCTGGAGAAAGTTCGGAAGATGTCATGATGAGCACGGCCTGTGGTTAAAGCAGGCCCTTG	1320
P G E S S E D V V M M S T P V V K A A L -		
1321	GAAATGGGCTTCAGTAGGAGCCTGGTGAAGACAGACGGTTCACTGGCAGATCCTGGCCACT	1380
E M G E S R S L V R Q T V Q W Q I L A T -		
1381	GGTGAGAACTACAGGACCGTCACTGACCTCGTTTACTCGATGCCAGAACGAGCAGAG	1440
G E N Y R T V S D L V I G L L D A E D E -		
1441	ATGAGAGGAGCAGATGGAGCAGGGGGCCGAGGAGGAGTCAGATGATCTAGCACTA	1500
M R E E Q M E Q A A E E E S D D L A L -		
1501	ATCCGGAAGAACAAATGGTGCTTTCCAACATTGACGCTGTGACACCAATGCTGTAT	1560
I R K N K M V L F Q H L T C V T P M L Y -		

Fig. 5 (page 4 of 6)

M-hiap-1

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M-hiap-1

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M-hiap-2

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M-hiap-2

GA~~C~~TGCTTCAGCCAGTCTGCAGTCTCCATCTAAGAATA~~T~~GTCTCCTGTGAAAAGTAG
421 ---+---+---+---+---+---+---+---+---+---+---+---+ 480
T L I S A S L Q S P S K N M S P V K S R -

AT~~T~~GCACATTCGT~~C~~ACCTCTGGAAC~~G~~AGGTGGCATTC~~A~~CT~~C~~AA~~C~~CTGTGCTCTAGGCC
481 ---+---+---+---+---+---+---+---+---+---+---+---+ 540
F A H S S P L E R G I H S N L C S S P -

TCTTAATTCTAGAGCAGTGGAAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
541 ---+---+---+---+---+---+---+---+---+---+---+---+ 600
L N S R A V E D F S S R M D P C S Y A M -

GAGTACAGAAGAGGCCAGATTCTACTTACAGTATGTGGCC~~T~~TAAGTTTCTGT~~C~~ACCC
601 ---+---+---+---+---+---+---+---+---+---+---+---+ 660
S T E E A R F L T Y S M W P L S F L S P -

AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCC~~T~~GGAGACAGGGCTGGCTGTTT
661 ---+---+---+---+---+---+---+---+---+---+---+---+ 720
A E I A R A G F Y Y I G P G D R V A C F -

TGCCTG~~T~~GGAAACTGAGCAA~~T~~GGAAACTGGGAA~~C~~AA~~G~~ATTATGCTATGT~~C~~AGAGGCC
721 ---+---+---+---+---+---+---+---+---+---+---+---+ 780
A C G G K L S N W E P K D Y A M S E H R -

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M-hiap-2

781 CAGACATTCCCCCACTGTC CATTCTGGAAAATACTTCAGAAAACAGAGGTTAGTAT
R H F P H C P F L E N T S E T Q R F S I - 840

841 ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGGAGACATTCTGTACTGCCACC
S N L S M Q T H S A R L R T F L Y W P P - 900

901 TAGTGGTTCCTGTTCAAGCCGGAGCCTTGCAAGTGGATTCTATTACGTGGATCGCRA
S V P V Q P E Q L A S A G F Y Y V D R N - 960

961 TGATGATGTC AAGTGCCTTGTGTGATGGGGCTTGAGATGTGGAACCTGGAGATGA
D D V K C L C C D G G L R C W E P G D D - 1020

1021 CCCCTGGATAAGAACACGCCAAATGGTTCCAAAGGTGTGAGTTCTTGATAACGGATGAAGGG
P W I E H A K W F P R C E F L I R M K G - 1080

1081 TCAGGAGTTGTTGATGAGATTCAAGCTAGATATCCTCATCTTGTGAGCAGCTGTGTC
Q E F V D E I Q A R Y P H L L E Q L L S - 1140

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CACTTCAGACACCCAGGAGAACAAATGCTGACCCCTACAGAGACAGTGGTGCATTGG
1141 T S D T P G E E N A D P T E T V V H F G - 1200

CCCTGGAGAAAGTCGAAAGATGTCGTCAATGAGGCACGCCCTGGTAAAGCAGCCTT
1201 P G E S S K D V V M M S T P V V K A A L - 1260

GGAAATGGGCTTCAGTAGGGCCTGGTGGAGACAGACGGTTCAAGGGCAGATCCTGGCAC
1261 E M G F S R S L V R Q T V Q R Q I L A T - 1320

TGGTGGAGAACTACAGGACCGTCAATGATAATTGTCTCAAGTCTGAATGCTGAAGATGA
1321 G E N Y R T V N D I V S V L L N A E D E - 1380

GAGAAGGAGGAGGAAAGAACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
1381 R R E E K E R Q T E E M A S G D L S L - 1440

GATTGGAGAAATAGAAATGGCCCTCTTCAACAGTTGACACATGTCCTCCATACCTGGGA
1441 I R K N R M A L E Q Q L T H V L P I L D - 1500

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M-hiap-2

TAATCTTGTAGGCCAGTGTAAATTACAAAACAGGAACATGATATTAGACAGAAAC
1501 - - - + - + - + - + - + - + - + - + - + - + - + - + 1560
N L E A S V I T K Q E H D I I R Q K T -

ACAGATAACCCTTACAAGCAAGAGAGCTTATTGACACCGTTAGTCAGGAAATGCTGC
1561 - - - + - + - + - + - + - + - + - + - + - + - + - + 1620
Q I P L Q A R E L I D T V L V K G N A A -

AGCCAACATCTTCAAAAACACTCTCTGAAGGAAATTGACTCCACGTTATATGAAAACCTATT
1621 - - - + - + - + - + - + - + - + - + - + - + - + - + 1680
A N I F K N S L K G I D S T L Y E N L F -

TGTGGAAAAGAATATGAAGTATATCCAACAGAACAGACGTTCAAGGCTATGGAAAGA
1681 - - - + - + - + - + - + - + - + - + - + - + - + - + 1740
V E K N M K Y I P T E D V S G L S L E E -

GCAGTTGGGAGATTACAAGAACGAAACTTGCAAAGTGTGTATGGACAGAGGTTTC
1741 - - - + - + - + - + - + - + - + - + - + - + - + - + 1800
Q L R R L Q E E R T C K V C M D R E V S -

TATTGTGTTCATCCGGTGGTCATCTAGTAGTGTCTGCCAGGAATGTGCCCTCTCTAAAG
1801 - - - + - + - + - + - + - + - + - + - + - + - + - + 1860
I V F I P C G H L V V C Q E C A P S L R -

Fig. 6 (page 5 of 6)

M-hiap-2

Fig. 6 (page 6 of 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus	Cp_iap	Cydia pomonella
	Op_iap	Orygia pseudotsugata
Human	xiap	IAP on X chromosome
	hiap1, hiap2	two different human IAP genes
Mouse	m-xiap	mouse homologue of human xiap gene
Insect	diap	Drosophila IAP gene, not clearly a homologue of xiap or hiap

Fig. 7

note on consensus:

The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

1	kaaRLgTYtn	WPvqf..leps	rMAasGFYYY	GrgDeVrCaf	CkveitnWvr	gDdpetdHkr	waPqCpFV
SEQ ID NO:11	Op_iap-1	eevRLntFek	WPvsf..lsp	tMAknGFYYY	GrsDeVrCaf	CkveimnWke	gEdpaadHkk
SEQ ID NO:14	Cp_iap-1	earLytFkd	WPnpn..ilpq	ALAKAGFYYY	nrlDhVkcw	CngviakWeK	wapqCpFV
SEQ ID NO:15	diap-2	earLytFkd	WPnpn..ilpq	ALAKAGFYYY	nrlDhVkcw	CngviakWeK	wapqCpFV
SEQ ID NO:16	m-xiap-1	efnRLktFan	FPssspvsas	TLARAGFLYT	GegDtVqCFS	ChaaIdrWqy	gDsaVgrHrr
SEQ ID NO:17	xiap-1	efnRLktFan	FPssspvsas	TLARAGFLYT	GegDtVrCFS	ChaaIdrWqy	gDsaVgrHrk
SEQ ID NO:18	hiap1-1	elyRMstYst	FPagvpvser	SLARAGFYYY	GvndKvKCFc	Cg1mldnWkr	gDspstekHkk
SEQ ID NO:19	hiap2-1	elyRMstYst	FPagvpvser	SLARAGFYYY	GvndKvKCFc	Cg1mldnWkr	lYpsCrFV
SEQ ID NO:20	m-xiap-2	earRLksFqn	WPdyah1tpr	elASAGLYYT	GadDqVqCFC	Cggk1knWep	lYpsCSFI
SEQ ID NO:21	xiap-2	earRLksFqn	WPdyah1tpr	elASAGLYYT	GigDqVqCFC	Cggk1knWep	lYpsCSFI
SEQ ID NO:22	hiap1-2	enARL1tFqt	WP..lLf1spt	dlARAGFYYY	GpgDrvacFa	Cggk1snWep	kDnamseHlr
SEQ ID NO:23	hiap2-2	earRLtYhm	WP..lLf1sps	elARAGFYYY	GpgDrvacFa	Cggk1snWep	kDdamsseHrr
SEQ ID NO:24	m-xiap-3	yearRtFgt	Wiysv..nke	qlARAGFYAl	GegDkVkcFh	Cggg1tdWkp	sEdpwedqHak
SEQ ID NO:25	xiap-3	yearRtFgt	Wiysv..nke	qlARAGFYAl	GegDkVkcFh	Cggg1tdWkp	sEdpwedqHak
SEQ ID NO:26	hiap1-3	haarRFktFfn	WPssv1vnpe	qlASAGFYYY	GnsDDvkCFC	Cdggl1rcWes	gDdpwvqHak
SEQ ID NO:27	hiap2-3	haarMRtFmy	WPssvvpqpe	qlASAGFYYY	GnDdvkCFC	CdgglrcWes	gDdpwvqHak
SEQ ID NO:28	Op_iap-2	earRLrtFae	WPrg1kqrpe	elaeAGFYFt	GqgDktrCFC	Cdggl1kdWep	dDapwqqHar
SEQ ID NO:29	Cp_iap-2	earRvkFhn	WPrcmkqrpe	qmAdAGFYFt	GygDntkCFy	Cdggl1kdWep	eDvpweqHvr
SEQ ID NO:30	diap-3	vdarRLrtFtd	WPisniqpas	alaQAGLYYq	kn9DqVrCfh	CniglrsWqk	eDepwieHak
SEQ ID NO:31	diap-1	esvRLatFge	WPlnapvsae	dLvnangFF..	GtwnmeaCdf	gDlvaerHrr	ssPiCSmV
SEQ ID NO:2	Consensus	---RL-TF--	WP-----	-LA-AGFYY-	G--D-V-CF-	C----W--	--P-C-FV

Fig. 8 (page 1 of 5)

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BIR 3

	301	350	400	450
cp-iap	qrpeQMDAG	FFYtGYGDnt	KCFYcdGGLk	dWepeDvPWe
diap	qpasalaqAG	LYYqk1GdqY	rCFhCnigLr	QHvrWFdrCa
m-xiap	VnKEQLARAG	FyalGeGDKV	KCFhcgGGlt	sWqkeDEPwf eHAkwsPkCq
xiap	VnKEQLARAG	FyalGeGDKV	KCFhcgGGlt	QHAKCYPgCK
hiap1	VnpeQLASAG	FYYvGnsDDv	KCFccdGGLr	QHAKWYPgCK
hiap2	VqpeQLASAG	FYYvGrSDDv	KCFgCdGGLr	QHAKWFPrcE
consensus	V--EQLA-AG	FYY-G-GD-V	KCF-C-GGL-	QHAKWFP-C-
351				
cp-iap	YVqlvKGGrDY	VqkVit...	...	
diap	FVllakGpAY	VseVlattaa	nassqpaTap	aptlq...
m-xiap	YlldeKGQEY	InnIhlthp.	LeEslgrTae	kt...
xiap	YllleqKGQEY	InnIhlths.	LeEclvrtTe	kt...
hiap1	YllrirKGQEY	IrqVqasyph	LlEqllstSD	spgdeneass
hiap2	FllirmKGQEF	VdeIqgrypn	LlEqllstSD	iihlePgedh
consensus	Yl	---KGQEY	---	ttgeenadpp
401				
cp-iap	..acVLPge..	
diap	..advLmdea	pakeAltLgi	dggyvVrnaiq	rKllssGcaF
m-xiap	kiDdtifqnP	mVqeAirMgf	sfkdkKktme	stldeLlhDi
xiap	riDdtifqnP	mVqeAirMgf	sfkdkKkime	lslevLliadL
hiap1	seDaIMmntP	vInaAvemgf	srslyVqqtvq	kslevlVadL
hiap2	seDaVMmntP	vVksaleMgf	nrdlVqqtvl	rlvndlVIDL
consensus	--D-V---P	-V--A--Mgf	---	skiltGenY
				ktvndiVsal
				-KI---G--Y
				----VK----
				-KI---G--Y
				----LV-DL

Fig. 8 (page 3 of 5)

Fig. 8 (sheet 4 of 5)

Ring Zinc Finger

	551	600	601	635
cp-iap	...tki	...qkmsvstpng	CA1SVdKCPM	CRKIVtsvI
diap	sniskitdei	...k	CAPSVanCPM	VYFS.
m-xiapk	CAeavdKCPM	tFLS*
xiapk	CAeavdKCPM	tFLS*
hiap1	lyehlfvqqd	ikyiptedvs	CytVItfnqk	tFMS*
hiap2	lyknlfvdkn	mkyiptedvs	CytVItfkqk	tFMS*
consensus	---	---	CRstIkgtv	tFLS*
			PCGHILVvCqe	CRGIIkgtv
			PCGHILVvCqe	tFLS.
			PCGHILV-C--	-FLS-

Fig. 8 (sheet 5 of 5)

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus	
Cp_iap	Cydia pomonella
Op_iap	Orgya pseudotsugata
Human	
xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes
Mouse	
m-xiap	mouse homologue of human xiap gene
Insect	
diap	Drosophila IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

1	Eq1rlqEer	tCKVCMdkev	svvF1PCGH1	vvCqeCApel	rkCPic
	Eq1rlpEer	tCKVCMdkev	siVFlPCGH1	w CkddCAPs1	rkCPic
	Eq1rlqEek	1sKICMdrni	aIVFfPCGH1	atCKqCAeav	dkCPmC
	Eq1rlqEek	1CKICMdrni	aIVFvPCGH1	vtCKqCAeav	dkCPmC
	Enrq1kDar	1CKVCLdeev	qVVFlPCGH1	atCnqCApev	anCPmC
	EkepgveDsk	1CKIClyveec	iVcFvPCGHV	vacAKCA1sv	dkCPmC
		1CKIClGack	tvcFvPCGHV	vacGkCAaggV	ttCPVC
		-CKICM-----	-V-F-PCGH-	--C--CA---	--CP-C
		E-----E---			

Fig. 9

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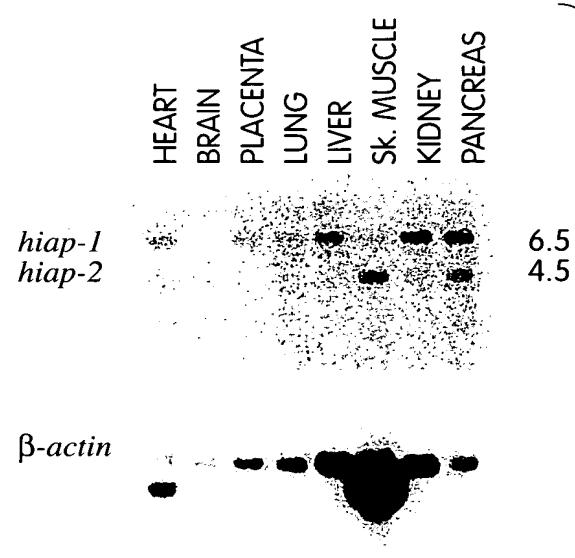


Fig. 10A

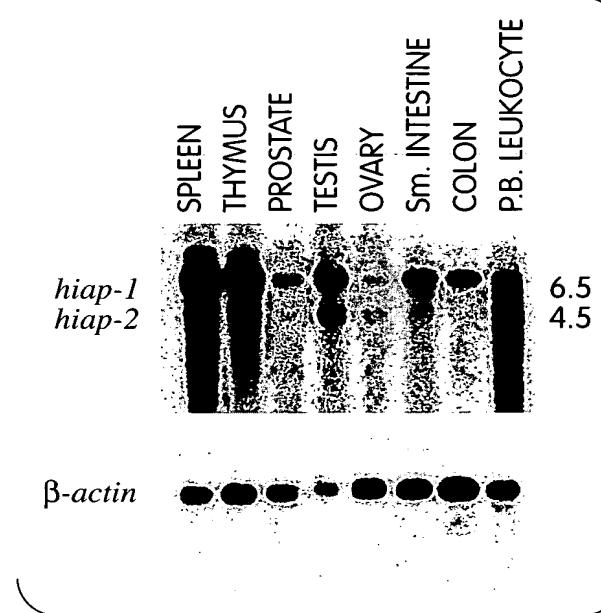


Fig. 10B

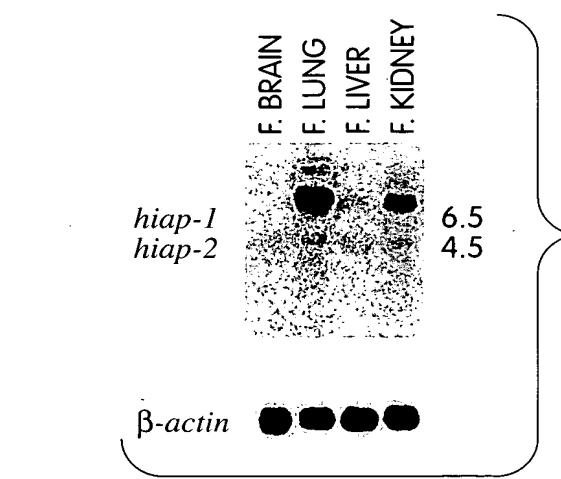


Fig. 10C

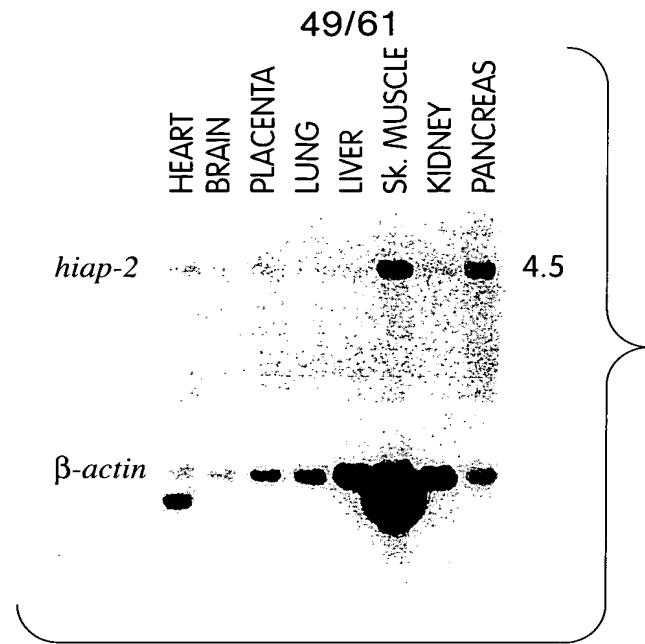


Fig. 11A

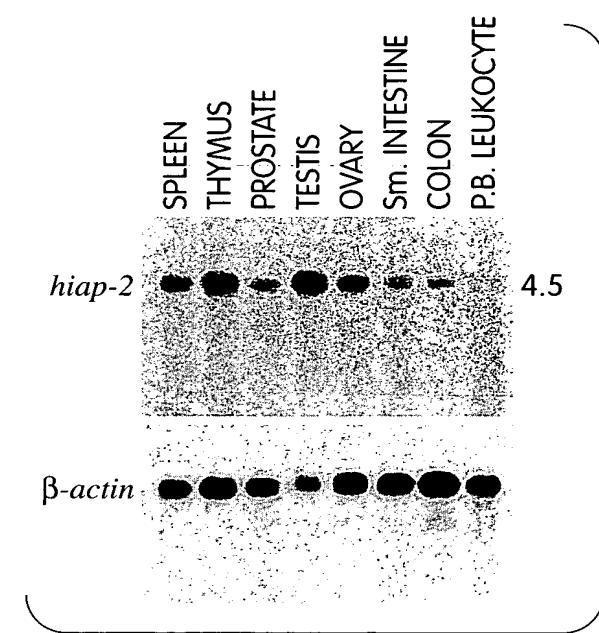


Fig. 11B

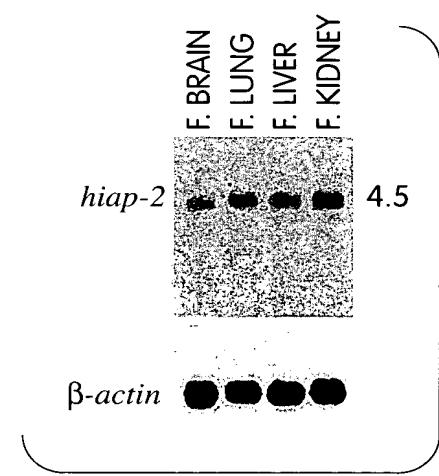


Fig. 11C

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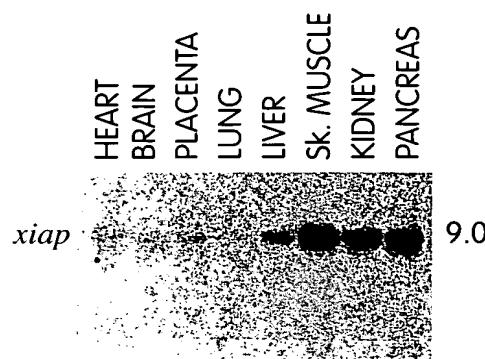


Fig. 12A

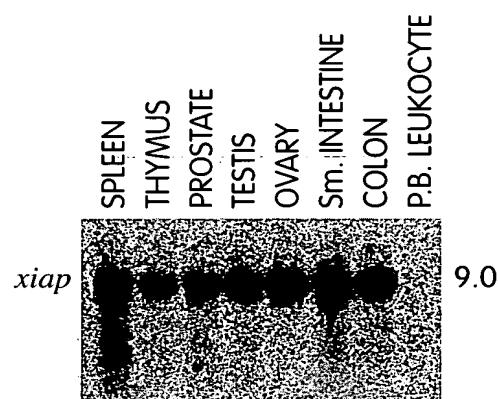


Fig. 12B

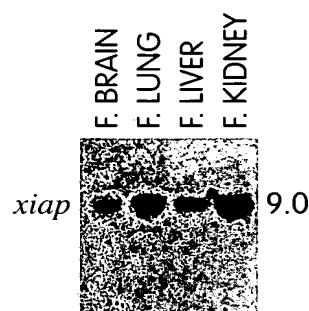


Fig. 12C



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S: STANDARDS

INCUBATION: OVERNIGHT

	Hg	CEM-CM ₃	GT/CEM	JKT				
HIV	- - +	- - +	- - +	- - +	- - +			
PHA/PMA	- + -	- - +	- - +	- - +	- - +			
S	+	-	+	-	+	-	-	S

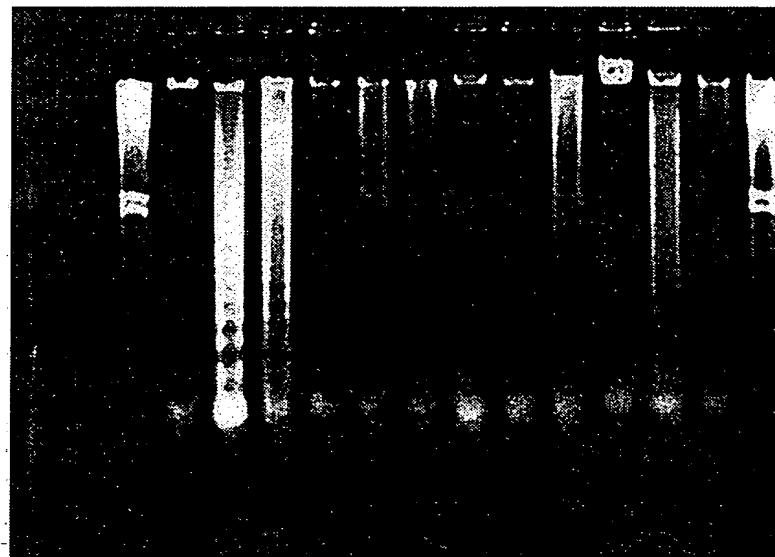


Fig. 13A

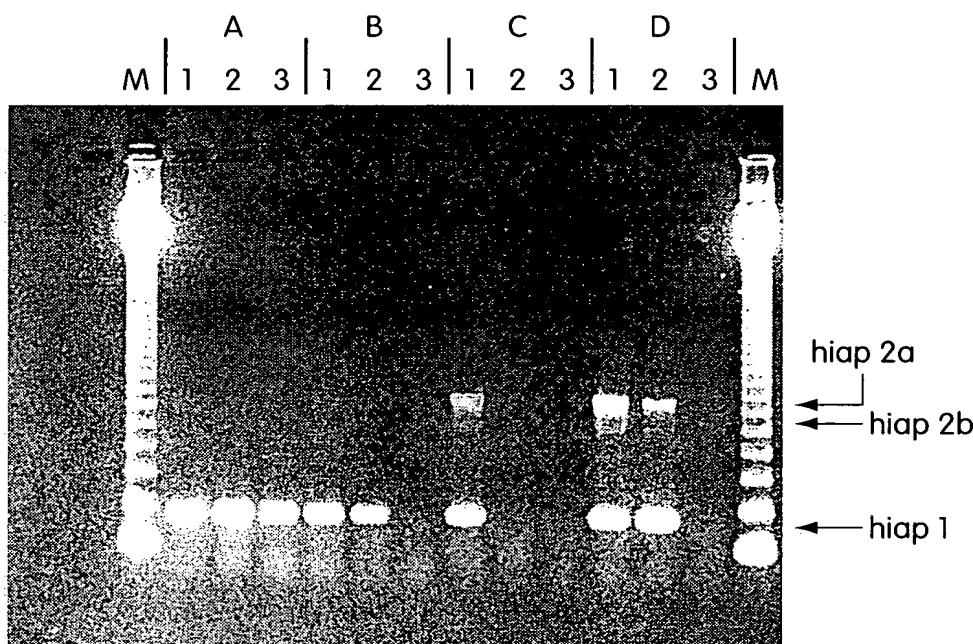


Fig. 13B

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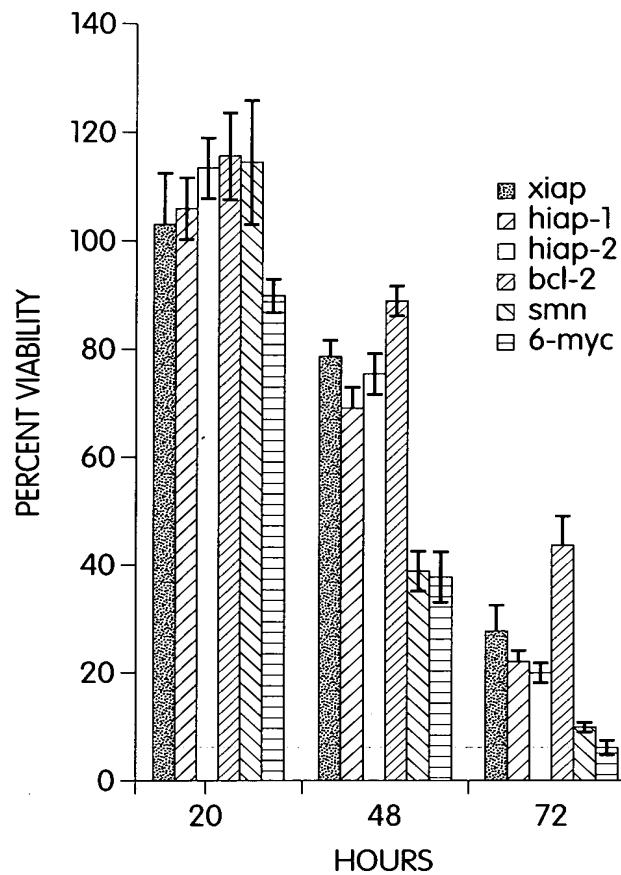


Fig. 14A

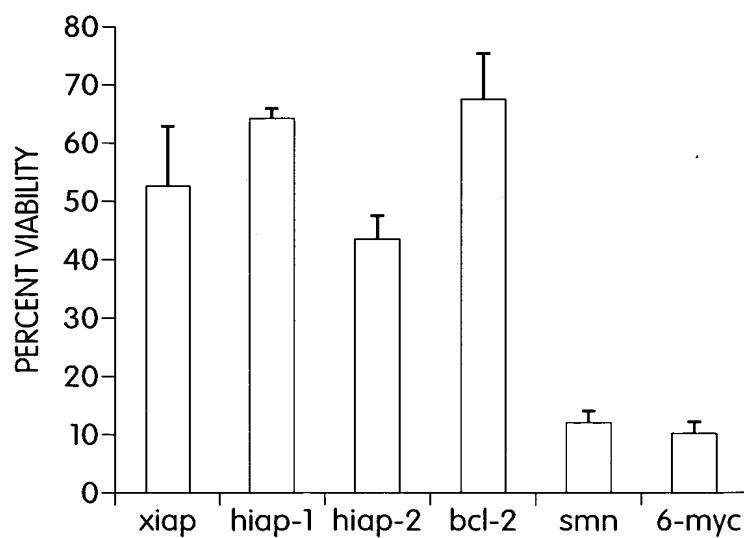


Fig. 14B

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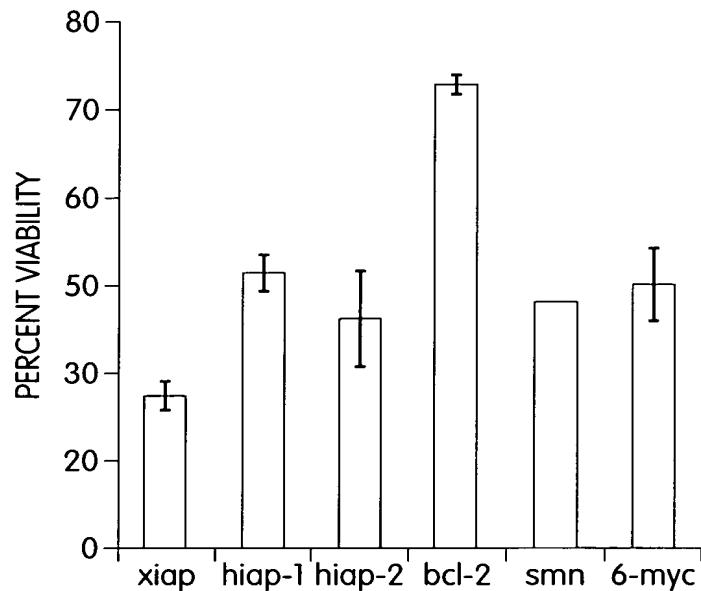


Fig. 14C

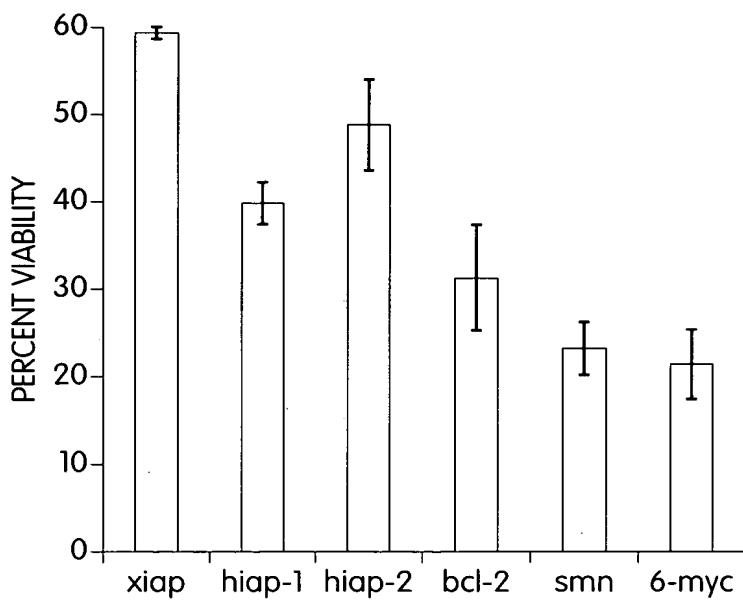
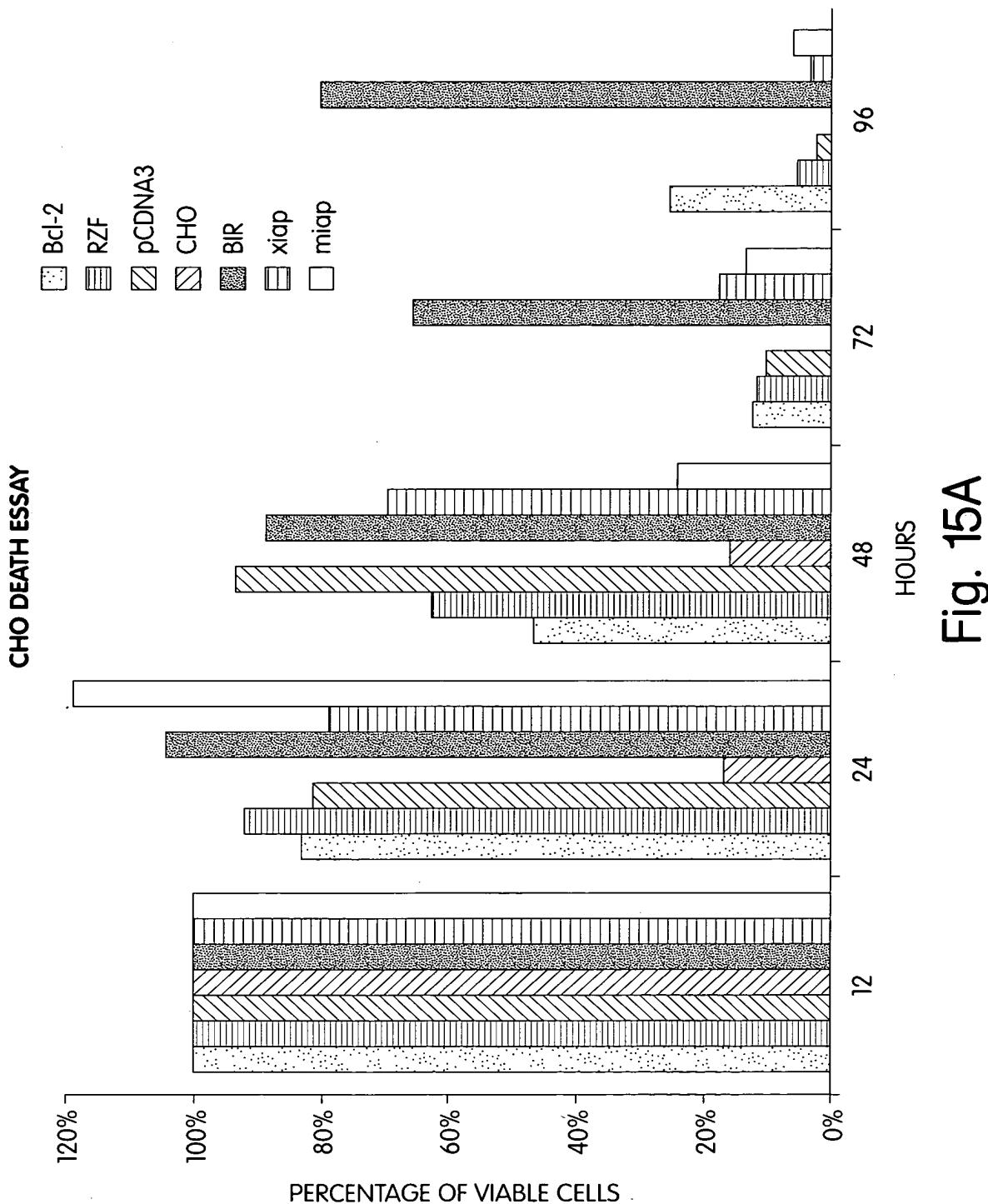


Fig. 14D



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CHO TRANSIENT DEATH ASSAY

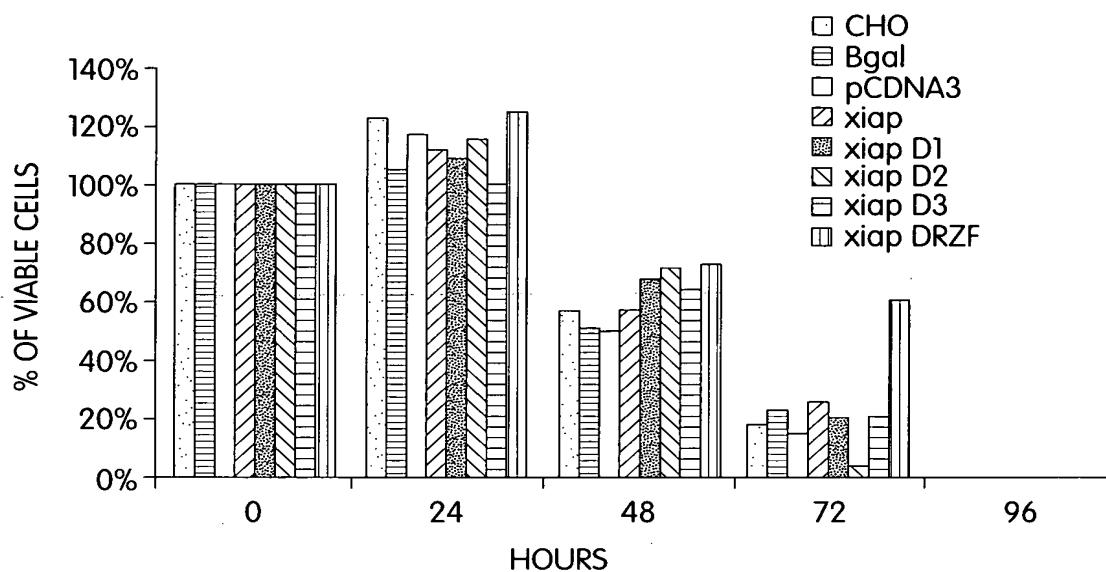


Fig. 15B

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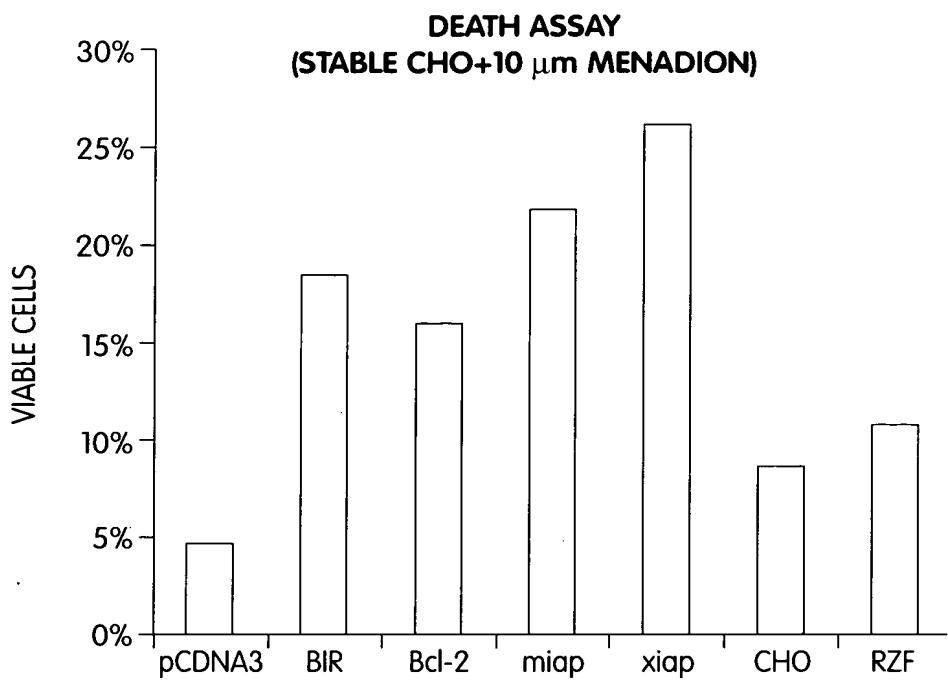


Fig. 16A

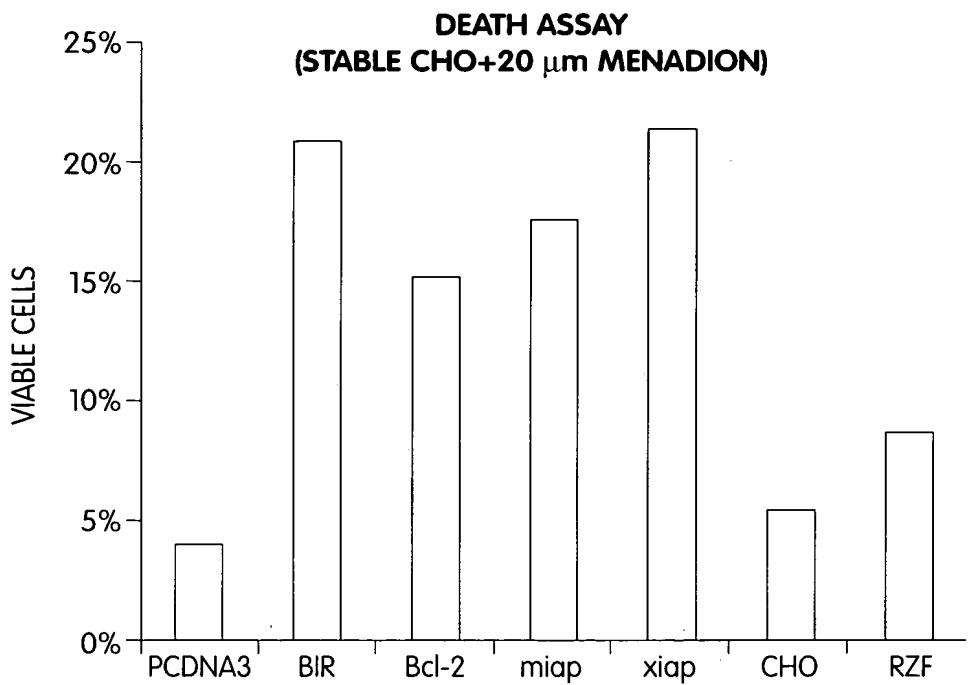


Fig. 16B

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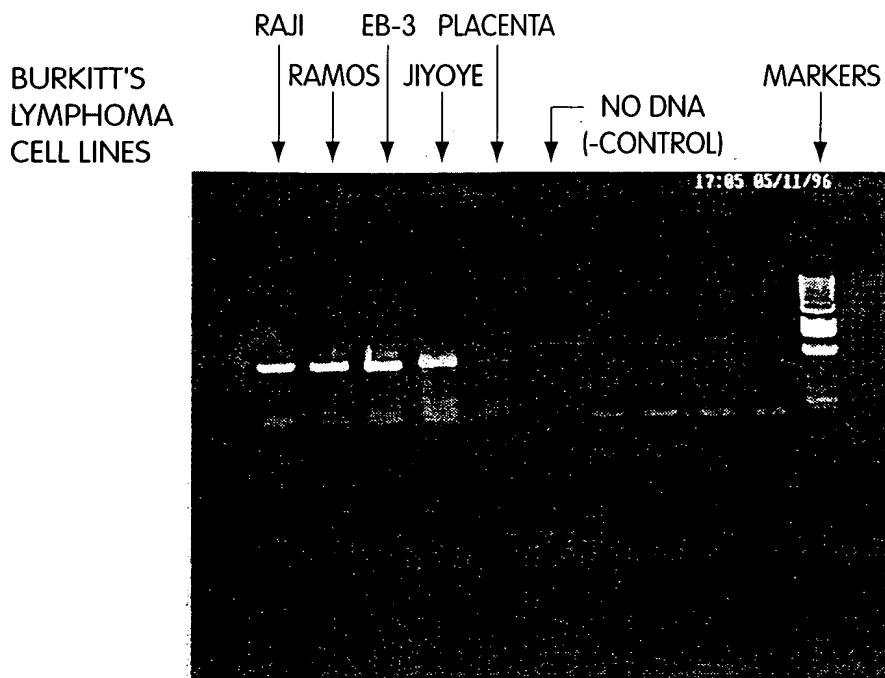


Fig. 17

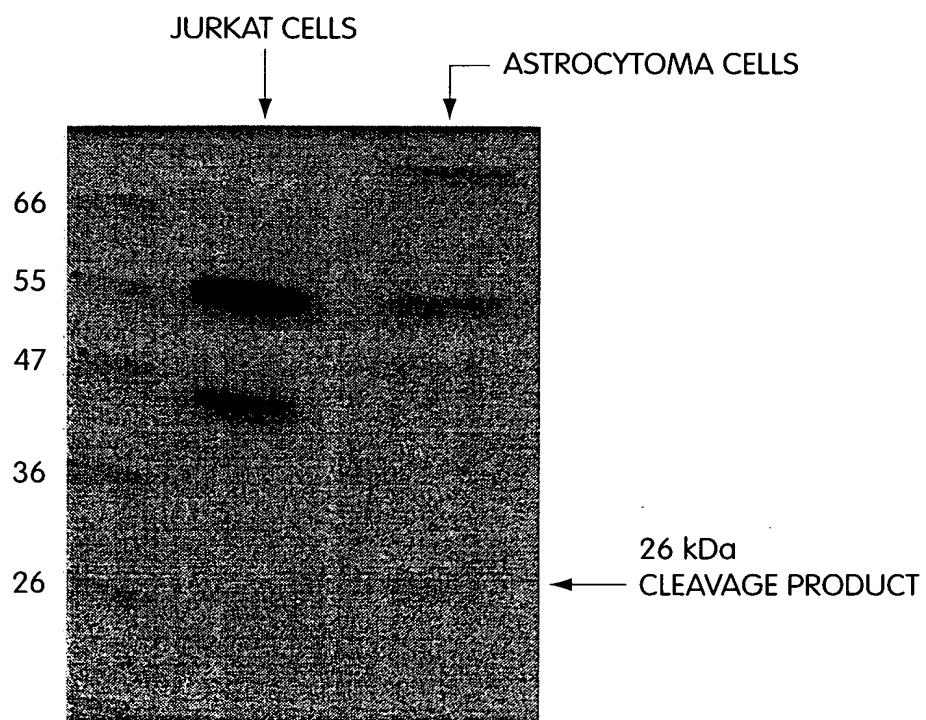


Fig. 18

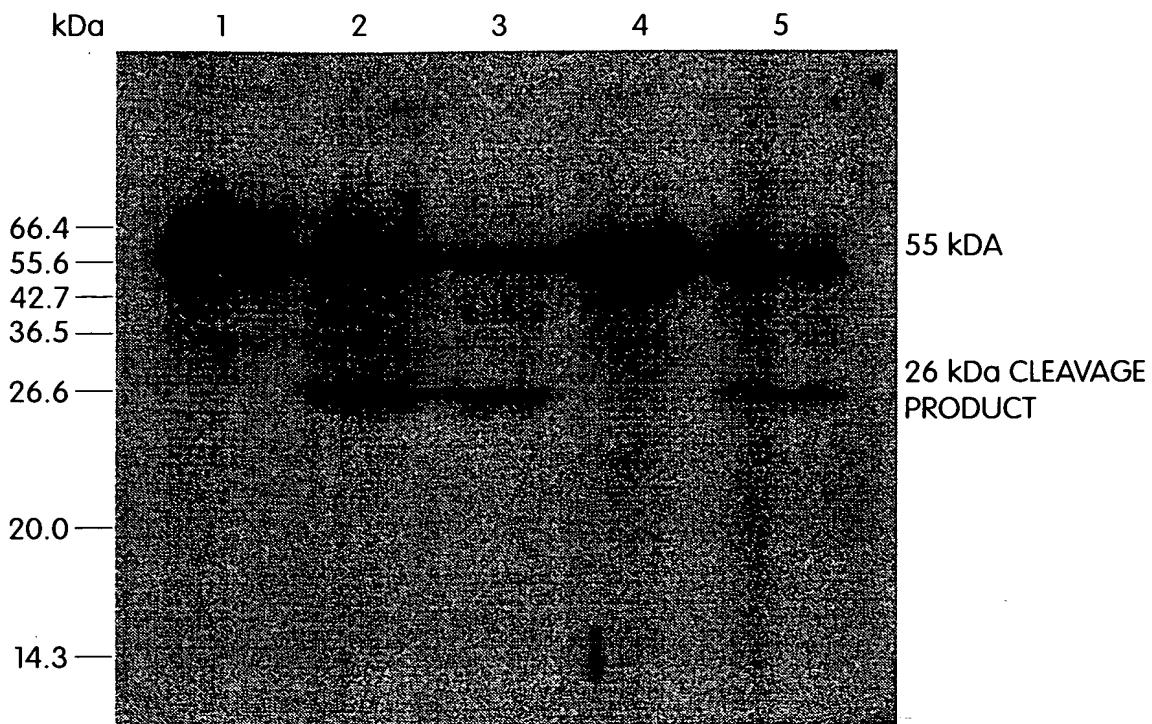


Fig. 19

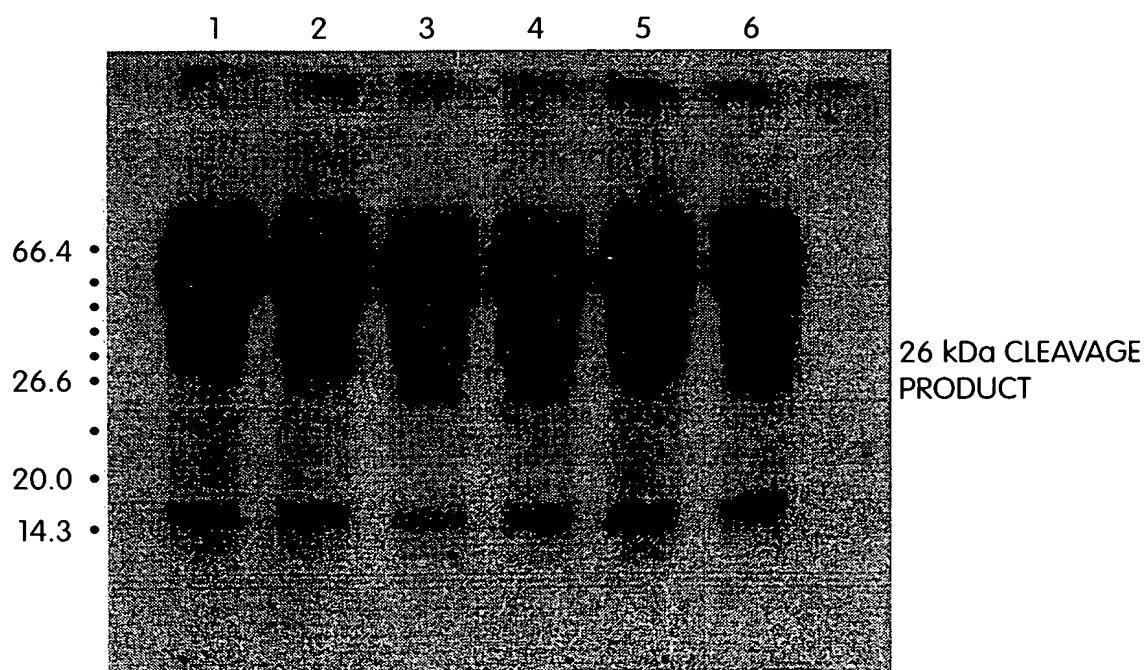


Fig. 20

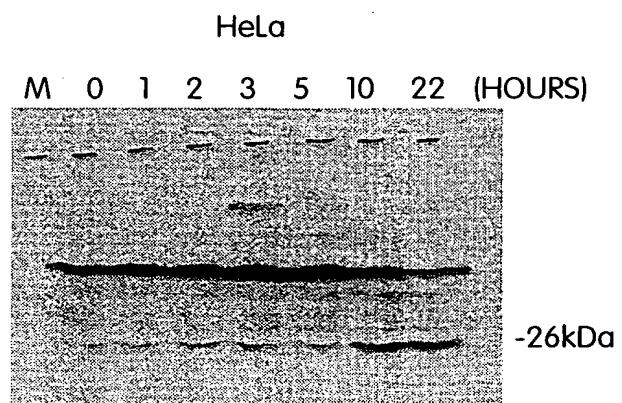


Fig. 21A

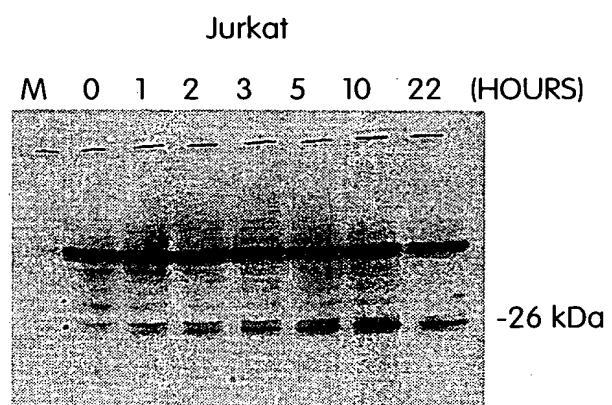


Fig. 21B

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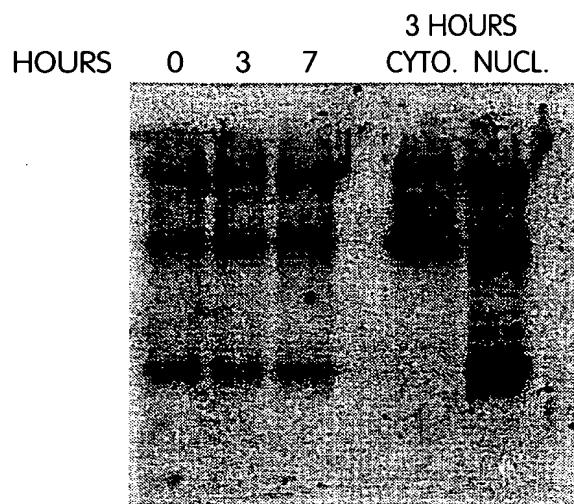


Fig. 22A

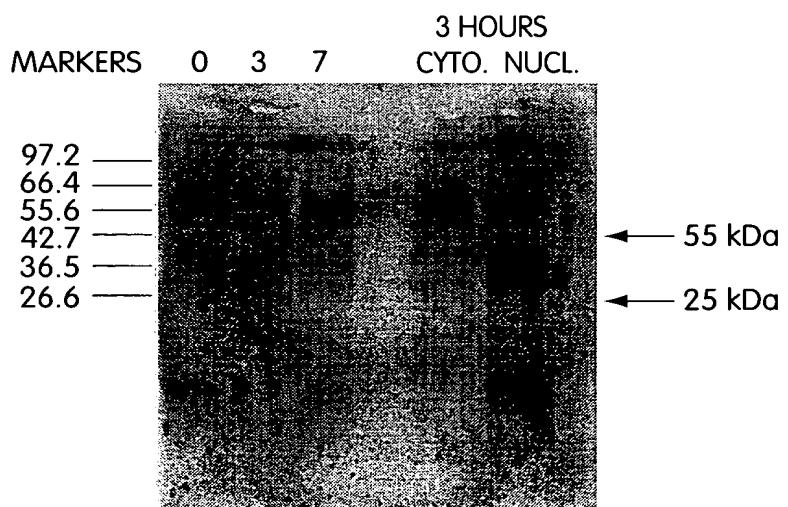


Fig. 22B

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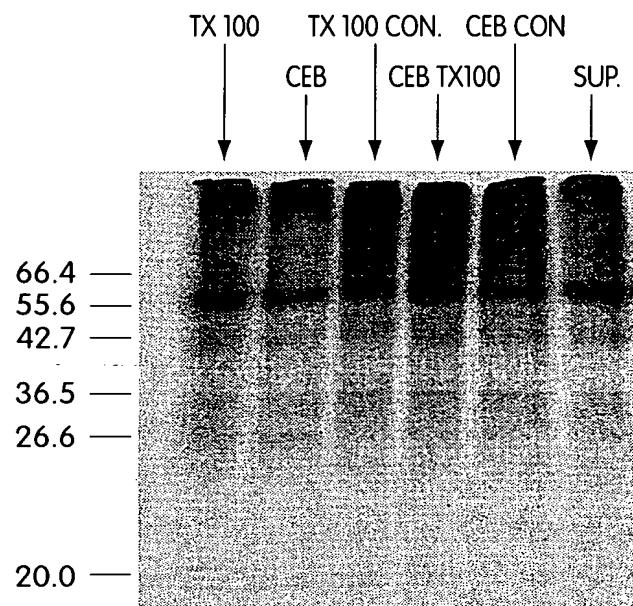


Fig. 23

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